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1600

## RAW SEQUENCE LISTING

DATE: 06/05/2002

PATENT APPLICATION: US/09/724,254A

TIME: 09:47:57

Input Set : A:\PTO.PG.txt

Output Set: N:\CRF3\06052002\I724254A.raw

p.6

3 <110> APPLICANT: Dalla-Favera, Riccardo  
5 <120> TITLE OF INVENTION: ISOLATION OF FIVE NOVEL GENES ENCODING FOR NEW Fc RECEPTORS-  
TYPE MELANOMA

ENTERED

6 INVOLVED IN THE PATHOGENESIS OF LYMPHOMA/MYELOMA  
8 <130> FILE REFERENCE: 0575/58044-a  
10 <140> CURRENT APPLICATION NUMBER: 09/724,254A  
11 <141> CURRENT FILING DATE: 2000-11-28  
13 <160> NUMBER OF SEQ ID NOS: 44  
15 <170> SOFTWARE: PatentIn version 3.1  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 515  
19 <212> TYPE: PRT  
20 <213> ORGANISM: Homo Sapiens  
22 <400> SEQUENCE: 1  
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25 1 5 10 15  
28 Ser Ala Ala Ala His Lys Pro Val Ile Ser Val His Pro Pro Trp Thr  
29 20 25 30  
32 Thr Phe Phe Lys Gly Glu Arg Val Thr Leu Thr Cys Asn Gly Phe Gln  
33 35 40 45  
36 Phe Tyr Ala Thr Glu Lys Thr Thr Trp Tyr His Arg His Tyr Trp Gly  
37 50 55 60  
40 Glu Lys Leu Thr Leu Thr Pro Gly Asn Thr Leu Glu Val Arg Glu Ser  
41 65 70 75 80  
44 Gly Leu Tyr Arg Cys Gln Ala Arg Gly Ser Pro Arg Ser Asn Pro Val  
45 85 90 95  
48 Arg Leu Leu Phe Ser Ser Asp Ser Leu Ile Leu Gln Ala Pro Tyr Ser  
49 100 105 110  
52 Val Phe Glu Gly Asp Thr Leu Val Leu Arg Cys His Arg Arg Arg Lys  
53 115 120 125  
56 Glu Lys Leu Thr Ala Val Lys Tyr Thr Trp Asn Gly Asn Ile Leu Ser  
57 130 135 140  
60 Ile Ser Asn Lys Ser Trp Asp Leu Leu Ile Pro Gln Ala Ser Ser Asn  
61 145 150 155 160  
64 Asn Asn Gly Asn Tyr Arg Cys Ile Gly Tyr Gly Asp Glu Asn Asp Val  
65 165 170 175  
68 Phe Arg Ser Asn Phe Lys Ile Ile Lys Ile Gln Glu Leu Phe Pro His  
69 180 185 190  
72 Pro Glu Leu Lys Ala Thr Asp Ser Gln Pro Thr Glu Gly Asn Ser Val  
73 195 200 205  
76 Asn Leu Ser Cys Glu Thr Gln Leu Pro Pro Glu Arg Ser Asp Thr Pro  
77 210 215 220  
80 Leu His Phe Asn Phe Phe Arg Asp Gly Glu Val Ile Leu Ser Asp Trp  
81 225 230 235 240

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84 Ser Thr Tyr Pro Glu Leu Gln Leu Pro Thr Val Trp Arg Glu Asn Ser
85                245                250                255
88 Gly Ser Tyr Trp Cys Gly Ala Glu Thr Val Arg Gly Asn Ile His Lys
89                260                265                270
92 His Ser Pro Ser Leu Gln Ile His Val Gln Arg Ile Pro Val Ser Gly
93                275                280                285
96 Val Leu Leu Glu Thr Gln Pro Ser Gly Gly Gln Ala Val Glu Gly Glu
97                290                295                300
100 Met Leu Val Leu Val Cys Ser Val Ala Glu Gly Thr Gly Asp Thr Thr
101 305                310                315                320
104 Phe Ser Trp His Arg Glu Asp Met Gln Glu Ser Leu Gly Arg Lys Thr
105                325                330                335
108 Gln Arg Ser Leu Arg Ala Glu Leu Glu Leu Pro Ala Ile Arg Gln Ser
109                340                345                350
112 His Ala Gly Gly Tyr Tyr Cys Thr Ala Asp Asn Ser Tyr Gly Pro Val
113                355                360                365
116 Gln Ser Met Val Leu Asn Val Thr Val Arg Glu Thr Pro Gly Asn Arg
117                370                375                380
120 Asp Gly Leu Val Ala Ala Gly Ala Thr Gly Gly Leu Leu Ser Ala Leu
121 385                390                395                400
124 Ile Leu Ala Val Ala Leu Leu Phe His Cys Trp Arg Arg Arg Lys Ser
125                405                410                415
128 Gly Val Gly Phe Leu Gly Asp Glu Thr Arg Leu Pro Pro Ala Pro Gly
129                420                425                430
132 Pro Gly Glu Ser Ser His Ser Ile Cys Pro Ala Gln Val Glu Leu Gln
133                435                440                445
136 Ser Leu Tyr Val Asp Val His Pro Lys Lys Gly Asp Leu Val Tyr Ser
137                450                455                460
140 Glu Ile Gln Thr Thr Gln Leu Gly Glu Glu Glu Glu Ala Asn Thr Ser
141 465                470                475                480
144 Arg Thr Leu Leu Glu Asp Lys Asp Val Ser Val Val Tyr Ser Glu Val
145                485                490                495
148 Lys Thr Gln His Pro Asp Asn Ser Ala Gly Lys Ile Ser Ser Lys Asp
149                500                505                510
152 Glu Glu Ser
153                515

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156 &lt;210&gt; SEQ ID NO: 2

157 &lt;211&gt; LENGTH: 2499

158 &lt;212&gt; TYPE: DNA

159 &lt;213&gt; ORGANISM: Homo Sapiens

161 &lt;400&gt; SEQUENCE: 2

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162 ctcaatcagc tttatgcaga gaagaagctt actgagctca ctgctggtgc tgggttaggc      60
164 aagtgcgtct ttggcaatct gggctgacct ggcttgcttc ctcagaactc cttctccaac      120
166 cctggagcag gcttccatgc tgctgtgggc gtccttgctg gcctttgctc cagtctgtgg      180
168 acaatctgca gctgcacaca aacctgtgat ttccgtccat cctccatgga ccacattctt      240
170 caaaggagag agagtgactc tgacttgcaa tggatttcag ttctatgcaa cagagaaaac      300
172 aacatggtat catcggcact actggggaga aaagttgacc ctgaccccag gaaacaccct      360
174 cgaggttcgg gaatctggac tgtacagatg ccaggcccgg ggctcccac gaagtaaccc      420
176 tgtgcgcttg ctcttttctt cagactcctt aatcctgcag gcaccatatt ctgtgtttga      480

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178 aggtgacaca ttggttctga gatgccacag aagaaggaaa gagaaattga ctgctgtgaa 540
180 atatacttgg aatggaaaca ttctttccat ttctaataaa agctgggatc ttcttatccc 600
182 acaagcaagt tcaaataaca atggcaatta togatgcatt ggatatggag atgagaatga 660
184 tgtattttaga tcaaatttca aaataattaa aattcaagaa ctatttccac atccagagct 720
186 gaaagctaca gactctcagc ctacagaggg gaattctgta aacctgagct gtgaaacaca 780
188 gcttctccca gagcggtcag acaccccaact tcaattcaac ttcttcagag atggcgaggt 840
190 catcctgtca gactggagca cgtaccogga actccagctc ccaaccgtct ggagagaaaa 900
192 ctcaggatcc tattggtgtg gtgctgaaac agtgaggggt aacatccaca agcacagtcc 960
194 ctcgctacag atccatgtgc agcggatccc tgtgtctggg gtgctcctgg agaccagcc 1020
196 ctcagggggc caggctgttg aaggggagat gctggtcctt gtctgctccg tggctgaagg 1080
198 cacaggggat accacattct cctggcaccg agaggacatg caggagagtc tggggaggaa 1140
200 aactcagcgt tccctgagag cagagctgga gctccctgcc atcagacaga gccatgcagg 1200
202 gggatactac tgtacagcag acaacagcta cggccctgtc cagagcatgg tgctgaatgt 1260
204 cactgtgaga gagaccccag gcaacagaga tggccttgtc gccgcgggag ccactggagg 1320
206 gctgctcagt gctcttctcc tggctgtggc cctgctgttt cactgctggc gtcggaggaa 1380
208 gtcaggagtt ggtttcttgg gagacgaaac caggctccct cccgctccag gccaggaga 1440
210 gtcctcccat tccatctgcc ctgcccaggt ggagcttcag tcgttgatg ttgatgtaca 1500
212 ccccaaaaag ggagatttgg tatactctga gatccagact actcagctgg gagaagaaga 1560
214 ggaagcta atccctcagga cacttctaga ggataaggat gtctcagttg tctactctga 1620
216 ggtaaagaca caaccccag ataactcagc tggaaagatc agctctaagg atgaagaaag 1680
218 ttaagagaat gaaaagttac gggaaagctc tactcatgtg atttctccct tgtccaaagt 1740
220 cccaggccca gtgcagtoct tgcggcacct ggaatgatca actcattcca gctttcta at 1800
222 tcttctcatg catatgcatt cactcccagg aatactcatt cgtctactct gatgttggga 1860
224 tggaatggcc tctgaaagac ttactaaaa tgaccaggat ccacagttaa gagaagaccc 1920
226 tgtagtattt gctgtgggcc tgacctaatg cattccctag ggtctgcttt agagaagggg 1980
228 gataaagaga gagaaggact gttatgaaaa acagaagcac aaatttttgt gaattgggat 2040
230 ttgcagagat gaaaaagact ggggtgacct gatctctgct taatacatct acaaccattg 2100
232 tctcactgga gactcacttg catcagtttg tttaactgtg agtggtgca caggcactgt 2160
234 gcaaacaatg aaaagccct tcaattctgc ctgcacagct tacactgtca ggattcagtt 2220
236 gcagattaaa gaaccatct ggaatggtt acagagagag gaatttaaaa gaggacatca 2280
238 gaagagctgg agatgcaagc tctaggctgc gcttccaaaa gcaaatgata attatgttaa 2340
240 tgtcattagt gacaaagatt tgcaacatta gagaaaagag acacaaatat aaaattaaaa 2400
242 acttaagtac caactctcca aaactaaatt tgaacttaaa atattagtat aaactcataa 2460
244 taaactctgc ctttaaataa aaaaaaaaaa aaaaaaaaaa 2499

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247 &lt;210&gt; SEQ ID NO: 3

248 &lt;211&gt; LENGTH: 592

249 &lt;212&gt; TYPE: PRT

250 &lt;213&gt; ORGANISM: Homo Sapiens

252 &lt;400&gt; SEQUENCE: 3

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254 Met Leu Leu Trp Val Ile Leu Leu Val Leu Ala Pro Val Ser Gly Gln
255 1 5 10 15
258 Phe Ala Arg Thr Pro Arg Pro Ile Ile Phe Leu Gln Pro Pro Trp Thr
259 20 25 30
262 Thr Val Phe Gln Gly Glu Arg Val Thr Leu Thr Cys Lys Gly Phe Arg
263 35 40 45
266 Phe Tyr Ser Pro Gln Lys Thr Lys Trp Tyr His Arg Tyr Leu Gly Lys
267 50 55 60
270 Glu Ile Leu Arg Glu Thr Pro Asp Asn Ile Leu Glu Val Gln Glu Ser
271 65 70 75 80

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274 Gly Glu Tyr Arg Cys Gln Ala Gln Gly Ser Pro Leu Ser Ser Pro Val
275      85      90      95
278 His Leu Asp Phe Ser Ser Ala Ser Leu Ile Leu Gln Ala Pro Leu Ser
279      100      105      110
282 Val Phe Glu Gly Asp Ser Val Val Leu Arg Cys Arg Ala Lys Ala Glu
283      115      120      125
286 Val Thr Leu Asn Asn Thr Ile Tyr Lys Asn Asp Asn Val Leu Ala Phe
287      130      135      140
290 Leu Asn Lys Arg Thr Asp Phe His Ile Pro His Ala Cys Leu Lys Asp
291 145      150      155      160
294 Asn Gly Ala Tyr Arg Cys Thr Gly Tyr Lys Glu Ser Cys Cys Pro Val
295      165      170      175
298 Ser Ser Asn Thr Val Lys Ile Gln Val Gln Glu Pro Phe Thr Arg Pro
299      180      185      190
302 Val Leu Arg Ala Ser Ser Phe Gln Pro Ile Ser Gly Asn Pro Val Thr
303      195      200      205
306 Leu Thr Cys Glu Thr Gln Leu Ser Leu Glu Arg Ser Asp Val Pro Leu
307      210      215      220
310 Arg Phe Arg Phe Phe Arg Asp Asp Gln Thr Leu Gly Leu Gly Trp Ser
311 225      230      235      240
314 Leu Ser Pro Asn Phe Gln Ile Thr Ala Met Trp Ser Lys Asp Ser Gly
315      245      250      255
318 Phe Tyr Trp Cys Lys Ala Ala Thr Met Pro His Ser Val Ile Ser Asp
319      260      265      270
322 Ser Pro Arg Ser Trp Ile Gln Val Gln Ile Pro Ala Ser His Pro Val
323      275      280      285
326 Leu Thr Leu Ser Pro Glu Lys Ala Leu Asn Phe Glu Gly Thr Lys Val
327      290      295      300
330 Thr Leu His Cys Glu Thr Gln Glu Asp Ser Leu Arg Thr Leu Tyr Arg
331 305      310      315      320
334 Phe Tyr His Glu Gly Val Pro Leu Arg His Lys Ser Val Arg Cys Glu
335      325      330      335
338 Arg Gly Ala Ser Ile Ser Phe Ser Leu Thr Thr Glu Asn Ser Gly Asn
339      340      345      350
342 Tyr Tyr Cys Thr Ala Asp Asn Gly Leu Gly Ala Lys Pro Ser Lys Ala
343      355      360      365
346 Val Ser Leu Ser Val Thr Val Pro Val Ser His Pro Val Leu Asn Leu
347      370      375      380
350 Ser Ser Pro Glu Asp Leu Ile Phe Glu Gly Ala Lys Val Thr Leu His
351 385      390      395      400
354 Cys Glu Ala Gln Arg Gly Ser Leu Pro Ile Leu Tyr Gln Phe His His
355      405      410      415
358 Glu Asp Ala Ala Leu Glu Arg Arg Ser Ala Asn Ser Ala Gly Gly Val
359      420      425      430
362 Ala Ile Ser Phe Ser Leu Thr Ala Glu His Ser Gly Asn Tyr Tyr Cys
363      435      440      445
366 Thr Ala Asp Asn Gly Phe Gly Pro Gln Arg Ser Lys Ala Val Ser Leu
367      450      455      460
370 Ser Ile Thr Val Pro Val Ser His Pro Val Leu Thr Leu Ser Ser Ala

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TIME: 09:47:57

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Output Set: N:\CRF3\06052002\I724254A.raw

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371 465          470          475          480
374 Glu Ala Leu Thr Phe Glu Gly Ala Thr Val Thr Leu His Cys Glu Val
375          485          490          495
378 Gln Arg Gly Ser Pro Gln Ile Leu Tyr Gln Phe Tyr His Glu Asp Met
379          500          505          510
382 Pro Leu Val Ser Ser Ser Thr Pro Ser Val Gly Arg Val Ser Phe Ser
383          515          520          525
386 Phe Ser Leu Thr Glu Gly His Ser Gly Asn Tyr Tyr Cys Thr Ala Asp
387          530          535          540
390 Asn Gly Phe Gly Pro Gln Arg Ser Glu Val Val Ser Leu Phe Val Thr
391 545          550          555          560
394 Gly Lys Cys Trp Val Leu Ala Ser Lys Pro Pro Leu Ala Glu Phe Ser
395          565          570          575
398 Leu Thr His Ser Phe Lys Asn Leu Phe Ala Leu Ser Ser Phe Leu Pro
399          580          585          590

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402 &lt;210&gt; SEQ ID NO: 4

403 &lt;211&gt; LENGTH: 5308

404 &lt;212&gt; TYPE: DNA

405 &lt;213&gt; ORGANISM: Homo Sapiens

407 &lt;400&gt; SEQUENCE: 4

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410 tcttttgatc tcagcccttg gtggtccagg tcttcatgct gctgtgggtg atattactgg      120
412 tcctggctcc tgtcagtgga cagtttgcaa ggacaccag gccattatt ttctccagc      180
414 tctccatgga ccacagtctt ccaaggagag agagtgacct tcacttgcaa gggatttcgc      240
416 tctactcacc acagaaaaca aaatggtacc atcggtagct tgggaaagaa atactaagag      300
418 aaaccccaga caatatcctt gagttcagga atctggagag tacagatgcc aggccaggg      360
420 ctcccctctc agtagccctg tgcacttgga tttttcttca gcttcgctga tcctgcaagc      420
422 tccactttct gtgtttgaag gagactctgt ggttctgagg tgccgggcaa aggcggaagt      480
424 aacctgaat aatactattt acaagaatga taatgtcctg gcattcctta ataaaagaac      540
426 tgacttccat attcctcatg catgtctcaa ggacaatggt gcatatcgct gtactggata      600
428 taaggaaaagt tgttgccctg tttcttccaa tacagtcaaa atccaagtcc aagagccatt      660
430 tacacgtcca gtgctgagag ccagctcctt ccagcccac agcggaacc cagtgacct      720
432 gacctgtgag acccagctct ctctagagag gtcagatgtc ccgctccggt tccgcttctt      780
434 cagagatgac cagaccctgg gattaggctg gagtctctcc ccgaatttcc agattactgc      840
436 catgtggagt aaagattcag ggttctactg gtgtaaggca gcaacaatgc ctcacagcgt      900
438 catatctgac agccccgaga tcttgatac aggtgcagat cctgcatct catcctgtcc      960
440 tctactctcag cctgaaaag gctctgaatt ttgagggaa caaggtgaca cttcactgtg      1020
442 aaacccagga agattctctg cgcactttgt acaggtttta tcatgagggt gtccccctga      1080
444 ggcacaagtc agtccgctgt gaaaggggag catccatcag cttctcactg actacagaga      1140
446 attcagggaa ctactactgc acagctgaca atggccttgg cgccaagccc agtaaggctg      1200
448 tgagcctctc agtcaactgt cccgtgtctc atcctgtcct caacctcagc tctcctgagg      1260
450 acctgatttt tgagggagcc aaggtgacac ttcactgtga agcccagaga ggttcaactcc      1320
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458 ctgtgtctca tctgtctctc accctcagct ctgctgaggc cctgactttt gaaggagcca      1560
460 ctgtgacact tcaactgtgaa gtccagagag gttccccaca aatcctatac cagttttatc      1620
462 atgaggacat gccctgtgg agcagctcaa caccctctgt ggggaagagt tccttcagct      1680
464 tctctctgac tgaaggacat tcagggaatt actactgcac agctgacaat ggctttggtc      1740

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/724,254A

DATE: 06/05/2002  
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Input Set : A:\PTO.PG.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:34; Xaa Pos. 25,26  
Seq#:37; Xaa Pos. 38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56  
Seq#:37; Xaa Pos. 57,58,59,60,61  
Seq#:38; Xaa Pos. 38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56  
Seq#:38; Xaa Pos. 57,58  
Seq#:39; Xaa Pos. 1,2,4,5,6

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5